FILE 'HOME' ENTERED AT 11:26:39 ON 15 FEB 2006

=> FILE MEDLINE, CAPLUS, BIOSIS
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.42	0.42

FILE 'MEDLINE' ENTERED AT 11:27:29 ON 15 FEB 2006

FILE 'CAPLUS' ENTERED AT 11:27:29 ON 15 FEB 2006

FILE 'BIOSIS' ENTERED AT 11:27:29 ON 15 FEB 2006

=> S ("type IIS restriction" OR "type 2S restriction") (S) (adapter OR linker OR primer OR tag)
L1 62 ("TYPE IIS RESTRICTION" OR "TYPE 2S RESTRICTION") (S) (ADAPTER OR LINKER OR PRIMER OR TAG)

=> DUP REM L1
PROCESSING COMPLETED FOR L1
L2 51 DUP REM L1 (11 DUPLICATES REMOVED)

=> S L AND PY<2004
L3 2659199 L AND PY<2004

=> S L2 AND PY<2004
L4 39 L2 AND PY<2004

=> D L4 1-10 IBIB ABS

L4 ANSWER 1 OF 39 MEDLINE on STN
ACCESSION NUMBER: 2003121495 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12433680
TITLE: Transcript profiling of human platelets using microarray and serial analysis of gene expression.
COMMENT: Comment in: Blood. 2003 Aug 15;102(4):1550-1. PubMed ID: 12900352
AUTHOR: Gnatenko Dmitri V; Dunn John J; McCorkle Sean R; Weissmann David; Perrotta Peter L; Bahou Wadie F
CORPORATE SOURCE: Department of Medicine, Program in Genetics, State University of New York, Stony Brook 11794-8151, USA.
CONTRACT NUMBER: HL49141 (NHLBI)
HL53665 (NHLBI)
M01 10710-5
SOURCE: Blood, **(2003 Mar 15)** 101 (6) 2285-93. Electronic Publication: 2002-11-14.
Journal code: 7603509. ISSN: 0006-4971.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200304
ENTRY DATE: Entered STN: 20030316
Last Updated on STN: 20030408
Entered Medline: 20030407

AB Human platelets are anucleate blood cells that retain cytoplasmic mRNA and maintain functionally intact protein translational capabilities. We have adapted complementary techniques of microarray and serial analysis of gene expression (SAGE) for genetic profiling of highly purified human blood

platelets. Microarray analysis using the Affymetrix HG-U95Av2 approximately 12 600-probe set maximally identified the expression of 2147 (range, 13%-17%) platelet-expressed transcripts, with approximately 22% collectively involved in metabolism and receptor/signaling, and an overrepresentation of genes with unassigned function (32%). In contrast, a modified SAGE protocol using the **Type IIS restriction** enzyme MmeI (generating 21-base pair [bp] or 22-bp **tags**) demonstrated that 89% of **tags** represented mitochondrial (mt) transcripts (enriched in 16S and 12S ribosomal RNAs), presumably related to persistent mt-transcription in the absence of nuclear-derived transcripts. The frequency of non-mt SAGE tags paralleled average difference values (relative expression) for the most "abundant" transcripts as determined by microarray analysis, establishing the concordance of both techniques for platelet profiling. Quantitative reverse transcription-polymerase chain reaction (PCR) confirmed the highest frequency of mt-derived transcripts, along with the mRNAs for neurogranin (NGN, a protein kinase C substrate) and the complement lysis inhibitor clusterin among the top 5 most abundant transcripts. For confirmatory characterization, immunoblots and flow cytometric analyses were performed, establishing abundant cell-surface expression of clusterin and intracellular expression of NGN. These observations demonstrate a strong correlation between high transcript abundance and protein expression, and they establish the validity of transcript analysis as a tool for identifying novel platelet proteins that may regulate normal and pathologic platelet (and/or megakaryocyte) functions.

L4 ANSWER 2 OF 39 MEDLINE on STN
ACCESSION NUMBER: 2002661789 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12421763
TITLE: Genomic signature tags (GSTs): a system for profiling genomic DNA.
AUTHOR: Dunn John J; McCorkle Sean R; Praissman Laura A; Hind Geoffrey; Van Der Lelie Daniel; Bahou Wadie F; Gnatenko Dmitri V; Krause Maureen K
CORPORATE SOURCE: Biology Department, Brookhaven National Laboratory, Upton, New York 11973, USA.. jdunn@bnl.gov
SOURCE: Genome research, **(2002 Nov)** 12 (11) 1756-65.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200301
ENTRY DATE: Entered STN: 20021108
Last Updated on STN: 20030115
Entered Medline: 20030114

AB Genomic signature tags (GSTs) are the products of a method we have developed for identifying and quantitatively analyzing genomic DNAs. The DNA is initially fragmented with a type II restriction enzyme. An oligonucleotide adaptor containing a recognition site for MmeI, a **type IIS restriction** enzyme, is then used to release 21-bp **tags** from fixed positions in the DNA relative to the sites recognized by the fragmenting enzyme. These tags are PCR-amplified, purified, concatenated, and then cloned and sequenced. The tag sequences and abundances are used to create a high-resolution GST sequence profile of the genomic DNA. GSTs are shown to be long enough for use as oligonucleotide primers to amplify adjacent segments of the DNA, which can then be sequenced to provide additional nucleotide information or used as probes to identify specific clones in metagenomic libraries. GST analysis of the 4.7-Mb Yersinia pestis EV766 genome using BamHI as the fragmenting enzyme and NlaIII as the tagging enzyme validated the precision of our approach. The GST profile predicts that this strain has several changes relative to the archetype CO92 strain, including deletion of a 57-kb region of the chromosome known to be an unstable pathogenicity

island.

L4 ANSWER 3 OF 39 MEDLINE on STN
ACCESSION NUMBER: 2001640678 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11691857
TITLE: SNP genotyping by multiplexed solid-phase amplification and fluorescent minisequencing.
AUTHOR: Shapero M H; Leuther K K; Nguyen A; Scott M; Jones K W
CORPORATE SOURCE: Affymax Inc., Palo Alto, California 94304, USA.
SOURCE: Genome research, **(2001 Nov)** 11 (11) 1926-34.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011107
Last Updated on STN: 20020730
Entered Medline: 20011207

AB The emerging role of single-nucleotide polymorphisms (SNPs) in clinical association and pharmacogenetic studies has created a need for high-throughput genotyping technologies. We describe a novel method for multiplexed genotyping of SNPs that employs PCR amplification on microspheres. Oligonucleotide PCR **primers** were designed for each polymorphic locus such that one of the **primers** contained a recognition site for BbvI (a **type IIS restriction** enzyme), followed by 11 nucleotides of locus-specific sequence, which reside immediately upstream of the polymorphic site. Following amplification, this configuration allows for any SNP to be exposed by BbvI digestion and interrogated via primer extension, four-color minisequencing. Primers containing 5' acrylamide groups were attached covalently to the solid support through copolymerization into acrylamide beads. Highly multiplexed solid-phase amplification using human genomic DNA was demonstrated with 57 beads in a single reaction. Multiplexed amplification and minisequencing reactions using bead sets representing eight polymorphic loci were carried out with genomic DNA from eight individuals. Sixty-three of 64 genotypes were accurately determined by this method when compared to genotypes determined by restriction-enzyme digestion of PCR products. This method provides an accurate, robust approach toward multiplexed genotyping that may facilitate the use of SNPs in such diverse applications as pharmacogenetics and genome-wide association studies for complex genetic diseases.

L4 ANSWER 4 OF 39 MEDLINE on STN
ACCESSION NUMBER: 1999403376 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10471752
TITLE: Tandem arrayed ligation of expressed sequence tags (TALEST): a new method for generating global gene expression profiles.
AUTHOR: Spinella D G; Bernardino A K; Redding A C; Koutz P; Wei Y; Pratt E K; Myers K K; Chappell G; Gerken S; McConnell S J
CORPORATE SOURCE: Chugai Biopharmaceuticals, Inc., 6275 Nancy Ridge Drive, San Diego, CA 92121, USA.. dspinella@chugaibio.com
SOURCE: Nucleic acids research, **(1999 Sep 15)** 27 (18) e22.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19990925
Last Updated on STN: 20010521
Entered Medline: 19990915

AB We have developed a new and simple method for quantitatively analyzing global gene expression profiles from cells or tissues. The process, called TALEST, or tandem arrayed ligation of expressed sequence **tags**, employs an oligonucleotide **adapter** containing a **type IIs restriction** enzyme site to facilitate the generation of short (16 bp) ESTs of fixed position in the mRNA. These ESTs are flanked by GC-clamped punctuation sequences which render them resistant to thermal denaturation, allowing their concatenation into long arrays and subsequent recognition and analysis by high-throughput DNA sequencing. A major advantage of the TALEST technique is the avoidance of PCR in all stages of the process and hence the attendant sequence-specific amplification biases that are inherent in other gene expression profiling methods such as SAGE, Differential Display, AFLP, etc. which rely on PCR.

L4 ANSWER 5 OF 39 MEDLINE on STN
ACCESSION NUMBER: 1999068507 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9853618
TITLE: Genotyping by mass spectrometric analysis of short DNA fragments.
COMMENT: Comment in: Nat Biotechnol. 1998 Dec;16(13):1314-5. PubMed ID: 9853606
AUTHOR: Laken S J; Jackson P E; Kinzler K W; Vogelstein B; Strickland P T; Groopman J D; Friesen M D
CORPORATE SOURCE: The Johns Hopkins Oncology Center, Baltimore, MD 21231, USA.
CONTRACT NUMBER: P01 ES06052 (NIEHS)
P30 CA06973 (NCI)
P30 ES03819 (NIEHS)
+
SOURCE: Nature biotechnology, **(1998 Dec)** 16 (13) 1352-6.
Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990226

AB A method has been developed to produce small DNA fragments from PCR products for analysis of defined DNA variations by mass spectrometry. The genomic region to be analyzed is PCR-amplified with **primers** containing a sequence for the **type IIS restriction** endonuclease Bpml. Bpml digestion of the resultant PCR products yields fragments as small as seven bases, which are then analyzed by electrospray ionization mass spectrometry. The approach was validated using seven different variants within the APC tumor suppressor gene, in which a perfect correlation was obtained with DNA sequencing. Both the sense and antisense strands were analyzed independently, and several variants can be analyzed simultaneously. These results provide the basis for a generally applicable and highly accurate method that directly queries the mass of variant DNA sequences.

L4 ANSWER 6 OF 39 MEDLINE on STN
ACCESSION NUMBER: 96299639 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8661003
TITLE: Mapping genomic library clones using oligonucleotide arrays.
AUTHOR: Sapolsky R J; Lipshutz R J
CORPORATE SOURCE: Affymetrix, 3380 Central Expressway, Santa Clara, California, 95051, USA.
CONTRACT NUMBER: F32-HG00105-03 (NHGRI)
R-R01-HG00813-03 (NHGRI)
SOURCE: Genomics, **(1996 May 1)** 33 (3) 445-56.

Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199609
ENTRY DATE: Entered STN: 19961008
Last Updated on STN: 19980206
Entered Medline: 19960920

AB We have developed a high-density DNA probe array and accompanying biochemical and informatic methods to order clones from genomic libraries. This approach involves a series of enzymatic steps for capturing a set of short dispersed sequence markers scattered throughout a high-molecular-weight DNA. By this process, all the ambiguous sequences lying adjacent to a given **Type IIS restriction** site are ligated between two DNA **adapters**. These markers, once amplified and labeled by PCR, can be hybridized and detected on a high-density oligonucleotide array bearing probes complementary to all possible markers. The array is synthesized using light-directed combinatorial chemistry. For each clone in a genomic library, a characteristic set of sequence markers can be determined. On the basis of the similarity between the marker sets for each pair of clones, their relative overlap can be measured. The library can be sequentially ordered into a contig map using this overlap information. This new methodology does not require gel-based methods or prior sequence information and involves manipulations that should allow for easy adaptation to automated processing and data collection.

L4 ANSWER 7 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:934235 CAPLUS
DOCUMENT NUMBER: 141:389803
TITLE: Genomic signature tag (GST) system for profiling genomic DNA and its use in diagnosis, metagenomics and forensic analysis
INVENTOR(S): Dunn, John J.; Van Der Lelie, Daniel; Krause, Maureen K.; McCorkle, Sean R.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 50 pp., Cont.-in-part of U.S. Ser. No. 113,916.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004219580	A1	20041104	US 2004-791074	20040302
US 2003186251	A1	20031002	US 2002-113916	20020401 <--

PRIORITY APPLN. INFO.: US 2002-113916 A2 20020401

AB Genomic signature tags (GSTs) are the products of a method developed for identifying and quant. analyzing genomic DNAs. The DNA is initially fragmented with a type II restriction enzyme. An oligonucleotide adaptor containing a recognition site for MmeI, a **type IIS restriction** enzyme, is then used to release **tags** from fixed positions in the DNA relative to the sites recognized by the fragmenting enzyme. These tags are PCR-amplified, purified, concatenated, and then cloned and sequenced. The tag sequences and abundances are used to create a high-resolution GST sequence profile of the genomic DNA. GSTs are shown to be long enough for use as oligonucleotide primers to amplify adjacent segments of the DNA, which can then be sequenced to provide addnl. nucleotide information or used as probes to identify specific clones in metagenomic libraries. Various embodiments of the invention described herein include methods for using single point genome signature

tags to analyze the related families present in a sample, methods for analyzing sequences associated with hyper- and hypo-methylated CpG islands, methods for visualizing organismic complexity change in a sampling location over time and methods for generating the genome signature tag profile of a sample of fragmented DNA.

L4 ANSWER 8 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:451553 CAPLUS
DOCUMENT NUMBER: 141:18700
TITLE: High throughput method for sequencing of genetic polymorphisms or mutations using loci-specific primers that create a restriction endonuclease cleavage site
INVENTOR(S): Dhallan, Ravinder S.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 82 pp., Cont.-in-part of U.S. Ser. No. 93,618.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004106102	A1	20040603	US 2003-376770		20030228
US 2003186239	A1	20031002	US 2002-93618		20020311 <--
US 6977162	B2	20051220			
US 2004137470	A1	20040715	US 2003-661165		20030911
US 2005260656	A1	20051124	US 2005-107624		20050415
PRIORITY APPLN. INFO.:			US 2002-360232P	P	20020301
			US 2002-93618	A2	20020311
			US 2002-378354P	P	20020508
			US 2003-376770	A2	20030228
			WO 2003-US6198	A2	20030228
			WO 2003-US27308	A1	20030829

AB The invention provides a method useful for determining the sequence of large nos. of loci of interest on a single or multiple chromosomes. The method utilizes an oligonucleotide primer that contains a recognition site for a restriction enzyme such that digestion with the restriction enzyme generates a 5' overhang containing the locus of interest. The 5' overhang is used as a template to incorporate nucleotides, which can be detected. The method is especially amenable to the anal. of large nos. of sequences, such as single nucleotide polymorphisms, from one sample of nucleic acid. The examples of the invention provide primers and methods for genotyping human SNPs (single nucleotide polymorphisms) and for detecting mutations in the human APC gene at codons 1302 and 1370 that are associated with colorectal cancer.

L4 ANSWER 9 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:796208 CAPLUS
DOCUMENT NUMBER: 139:302973
TITLE: Method for generating five prime biased tandem tag libraries of cDNAs from mammals
INVENTOR(S): Samal, Babru; Li, Yuan; Hermida, Leandro C.; Hoppa, Nancy L.; Johe, Karl K.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 23 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

US 2003190618	A1	20031009	US 2002-92885	20020306 <--
PRIORITY APPLN. INFO.:			US 2002-92885	20020306

AB A method for generating five prime biased tandem tag libraries of cDNAs is revealed. The method allows generation of partial sequences consisting of a minimal length of expressed cDNA sequences of at least 20 bases from biol. samples to rapidly identify novel expressed transcripts. The steps of include: (a) isolating a sample of mRNAs; (b) synthesizing double-stranded cDNAs from the mRNAs; (c) blunt-ending the double-stranded cDNAs; (d) attaching an **adapter** mol. to the blunt ends of the double stranded cDNAs to form a complex, wherein the **adapter** mol. is a double stranded synthetic oligonucleotide; (e) digesting the complex with a **type IIS restriction** enzyme to form released **tags**; (f) separating the released **tags** from the double-stranded cDNAs; (g) amplifying the released **tags** to form amplified **tags**; (h) isolating the amplified **tags** ; (i) concatenating the amplified **tags** to form concatenated **tags**; (j) amplifying the concatenated **tags**; and (k) isolating the concatenated **tags**. The **adapter** mol. comprises: (1) a recognition site for a **type IIS restriction** enzyme, (2) a cloning site for releasing **tags** to a cloning vector, and (3) a PCR **primer** site.

L4 ANSWER 10 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:777243 CAPLUS
DOCUMENT NUMBER: 139:287255
TITLE: Construction of genomic signature tag (GST) system for profiling microbial genomic DNA
INVENTOR(S): Dunn, John J.; Van der Lelie, Daniel; Krause, Maureen K.
PATENT ASSIGNEE(S): Brookhaven Science Associates, LLC, USA
SOURCE: U.S. Pat. Appl. Publ., 12 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003186251	A1	20031002	US 2002-113916	20020401 <--
US 2004219580	A1	20041104	US 2004-791074	20040302
PRIORITY APPLN. INFO.:			US 2002-113916 A2	20020401

AB Genomic Signature Tags (GSTs) are the products of a method for identifying and quant. analyzing genomic DNAs. The DNA is initially fragmented with a type II restriction enzyme and the fragments are then ligated with biotinylated duplex linker, digested with NlaIII enzyme and captured with streptavidin-coated magnetic beads. An oligonucleotide **adapter** containing a recognition site for MmeI, a **type IIS restriction** enzyme, is then used to release 21 bp **tags** from fixed positions in the DNA relative to the sites recognized by the fragmenting enzyme. These tags are PCR-amplified, purified, concatenated into longer mols., and then cloned and sequenced. The tag sequences and abundances are used to create a GST profile that can identify and quantify the genome of origin within any complex DNA isolate. The total number of GSTs generated from a sample is determined by the incidence of recognition sites for the initial fragmenting enzyme.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	42.72	43.14

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE ENTRY TOTAL SESSION

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Feb 10, 2006 (20060210/UP).

=>
=>
=> FILE MEDLINE, CAPLUS, BIOSIS

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	3.78	46.92

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-3.00

FILE 'MEDLINE' ENTERED AT 12:10:43 ON 15 FEB 2006

FILE 'CAPLUS' ENTERED AT 12:10:43 ON 15 FEB 2006
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=> D L4 11-20 IBIB ABS

L4 ANSWER 11 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:719652 CAPLUS
DOCUMENT NUMBER: 139:241304
TITLE: Detecting genome-wide sequence variations associated with a phenotype by correlation of restriction sequence tag variations with specific phenotypes
INVENTOR(S): Mayer, Pascal; Leviev, Ilia; Osteras, Magne; Farinelli, Laurent
PATENT ASSIGNEE(S): Manteia S.A., Switz.; Lee, Nicholas John
SOURCE: PCT Int. Appl., 117 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003074734	A2	20030912	WO 2003-GB941	20030305 <--
WO 2003074734	A3	20040219		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,

BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2004002090	A1	20040101	US 2003-378688	20030304
CA 2478722	AA	20030912	CA 2003-2478722	20030305 <--
AU 2003208480	A1	20030916	AU 2003-208480	20030305 <--
EP 1483404	A2	20041208	EP 2003-706768	20030305

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

JP 2005518811	T2	20050630	JP 2003-573179	20030305

PRIORITY APPLN. INFO.:

GB 2002-5153	A	20020305
US 2002-362023P	P	20020305
WO 2003-GB941	W	20030305

AB The invention provides methods for determining genome-wide sequence variations associated with phenotype of a species in a hypothesis-free manner. In the methods of the invention, a set of restriction fragments for each of a sub-population of individuals having the phenotype are generated by digesting nucleic acids from the individual using one or more different restriction enzymes. A set of restriction sequence tags for the individual is then determined from the set of restriction fragments. The restriction sequence tags for the sub-population of organisms are compared and grouped into one or more groups, each of which comprising restriction sequence tags that comprise homologous sequences. The obtained one or more groups of restriction sequence tags identify the sequence variations associated with the phenotype. The methods of the invention can be used for, e.g., anal. of large nos. of sequence variants in many patient samples to identify subtle genetic risk factors.

L4 ANSWER 12 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:697096 CAPLUS
DOCUMENT NUMBER: 139:225453
TITLE: Analysis of DNA populations using double digestion with type IIS restriction endonucleases as fingerprint
INVENTOR(S): Fischer, Achim
PATENT ASSIGNEE(S): Axaron Bioscience A.-G., Germany
SOURCE: PCT Int. Appl., 84 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003072819	A2	20030904	WO 2003-EP2032	20030227 <--
WO 2003072819	A3	20040722		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

DE 10208333	A1	20030904	DE 2002-10208333	20020227 <--
CA 2480320	AA	20030904	CA 2003-2480320	20030227 <--
AU 2003210377	A1	20030909	AU 2003-210377	20030227 <--
EP 1492888	A2	20050105	EP 2003-742963	20030227

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

US 2006029937	A1	20060209	US 2004-504847	20041001

PRIORITY APPLN. INFO.:

DE 2002-10208333	A	20020227
WO 2003-EP2032	W	20030227

AB A method of characterizing a DNA sample using the pattern of digestion

from two or more type IIS restriction endonucleases (cutting outside their recognition site) is described. Fragments are characterized by a simple test, such as determination of terminal bases and fragment length. The method may be used to process large nos. of samples in parallel. The sample may be characterized in a number of ways, such as cloning of fragments that will ligate to a limited number of adapters or are amplified by specific primer pairs.

L4 ANSWER 13 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:360780 CAPLUS
DOCUMENT NUMBER: 138:380357
TITLE: PCR-free cDNA cloning and cDNA library preparation method for gene expression analysis
INVENTOR(S): Yamamoto, Mikio
PATENT ASSIGNEE(S): Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 20 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2003135071	A2	20030513	JP 2001-336081	20011101 <--

PRIORITY APPLN. INFO.: JP 2001-336081 20011101
AB A method for cDNA cloning and cDNA library preparation without using polymerase chain reaction (PCR) is disclosed. The method comprises preparation of double-stranded cDNA, cleavage with type II restriction enzyme, ligation of **linker** DNA having **type IIs** **restriction** enzyme cleavage sites and a unique type II restriction enzyme cleavage site, cleavage with the 3rd **type IIs** **restriction** enzyme, purification of DNA fragments, ligation of another **linker** DNA, and transformation of E. coli competent cells with the plasmid vector prepared Use of the method for anal. of gene expression is claimed.

L4 ANSWER 14 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:221799 CAPLUS
DOCUMENT NUMBER: 138:249721
TITLE: Identification and quantification of nucleic acids by the production and serial sequencing of tags generated with BcgI-like restriction endonucleases
INVENTOR(S): Fischer, Achim
PATENT ASSIGNEE(S): Germany
SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003022986	A2	20030320	WO 2002-EP10016	20020906 <--
WO 2003022986	A3	20040108		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
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DE 10144132 A1 20030327 DE 2001-10144132 20010907 <--

PRIORITY APPLN. INFO.: DE 2001-10144132 A 20010907

AB The invention relates to a method for the identification and quantification of nucleic acids in a mixture, more particularly for determining gene expression data, splicing data or sequence variations, wherein the double-strand nucleic acids are spliced with a BcgI-like restriction endonuclease in order to produce nucleic acid tags of identical length. The method uses unique sequence tags of a uniform length generated using type restriction endonucleases similar to BcgI in their cleavage sites and cleavage products. These enzymes release oligonucleotides long enough to be unique to a gene within a complex genome. Alternatively, combinations of type II and type IIs restriction endonucleases may be used. The released nucleic acid tags are optionally isolated, the nucleic acid tags produced with the BcgI-like restriction endonucleases are concatemerized, cloned in a vector and then serially sequenced.

L4 ANSWER 15 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:203279 CAPLUS
DOCUMENT NUMBER: 138:232946
TITLE: Enzymatic synthesis of error-free oligonucleotide tags
INVENTOR(S): Brenner, Sydney; Williams, Steven R.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 22 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003049616	A1	20030313	US 2001-756830	20010108 <--

PRIORITY APPLN. INFO.: US 2001-756830 20010108

AB The invention provides oligonucleotide tag compns. and methods for synthesizing repertoires of error-free oligonucleotide tags that may be used for labeling and sorting polynucleotides, such as cDNAs, restriction fragments, and the like. In accordance with the method of the invention, oligonucleotide tag precursors are provided in an amplicon, wherein the tag precursors each consists of one or more oligonucleotide "words" selected from the same minimally cross-hybridizing set of words. The oligonucleotide tag precursors are elongated by repeated cycles of cleavage, ligation of one or more words, and amplification. Cycles continue until the oligonucleotide tags of the repertoire have a desired length or complexity.

L4 ANSWER 16 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:186672 CAPLUS
TITLE: Efficient biological construction of repetitive polypeptides for interconnect applications by block copolymerization
AUTHOR(S): Higashiya, Seiichiro; Ngo, Silvana C.; Bousman, Kenneth S.; Jin, Xiaolin; Welch, John T.; Cunningham, Richard P.; Eisenbraun, Eric T.; Geer, Robert E.; Kaloyeros, Alain E.
CORPORATE SOURCE: Department of Chemistry, University at Albany - SUNY, Albany, NY, 12222, USA
SOURCE: Abstracts of Papers, 225th ACS National Meeting, New Orleans, LA, United States, March 23-27, 2003 (**2003**), POLY-519. American Chemical Society: Washington, D. C.
CODEN: 69DSA4

DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB Self-assembly is an especially attractive strategy for the assembly of microstructures for microelectronics in the era of giga to tera scale integration. Our research involves the preparation of nanoscale mol. interconnects via precisely arrayed aromatic moieties utilizing the β-sheeted repetitive polypeptides pioneered by D. A. Tirrell et al. as scaffolds. Repetitive polypeptides were biol. generated from artificial coding sequences constructed by an improved block copolymn. technique. Monomeric DNA coding sequences and **adapters** possessing appropriately designed **type IIs** **restriction** endonuclease sites were ligated in unidirectional head-to-tail manner. The resultant oligomers bearing the appropriate restriction sites were cloned into plasmid vectors. The purely repetitive DNA sequences were recovered as oligomerized units by digestion using type IIs restriction endonucleases and used for longer multimer construction or block copolymn. with a second multimer unit. The DNA sequences so constructed were subcloned into expression vectors and the encoded polypeptides were overexpressed in E. coli hosts.

L4 ANSWER 17 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:76978 CAPLUS
DOCUMENT NUMBER: 138:148637
TITLE: Method for nucleic acid amplification by repetitive nicking-extension reactions and its use for sequence analysis of defined locations in target DNA
INVENTOR(S): Van Ness, Jeffrey; Galas, David J.; Van Ness, Lori K.
PATENT ASSIGNEE(S): Keck Graduate Institute, USA; Gowshall, Jon V.
SOURCE: PCT Int. Appl., 307 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008642	A2	20030130	WO 2002-GB3237	20020715 <--
WO 2003008642	A3	20030731		
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CA 2492007	AA	20030130	CA 2002-2492007	20020715 <--
CA 2492032	AA	20030814	CA 2002-2492032	20020715 <--
US 2003152952	A1	20030814	US 2002-197616	20020715 <--
US 6884586	B2	20050426		
WO 2003080645	A2	20031002	WO 2002-US22674	20020715 <--
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CA 2492423		AA	20040318	CA 2002-2492423	20020715
EP 1409732		A2	20040421	EP 2002-743441	20020715
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EP 1470250		A2	20041027	EP 2002-804810	20020715
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EP 1470251		A2	20041027	EP 2002-804811	20020715
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK					
JP 2004535815		T2	20041202	JP 2003-514957	20020715
BR 2002011155		A	20050201	BR 2002-11155	20020715
JP 2005516610		T2	20050609	JP 2003-566153	20020715
JP 2005519643		T2	20050707	JP 2004-569980	20020715
ZA 2004001157		A	20041019	ZA 2004-1157	20040212
PRIORITY APPLN. INFO.:				US 2001-305637P	P 20010715
				US 2002-345445P	P 20020102
				US 2001-331687P	P 20011119
				WO 2002-GB3237	W 20020715
				WO 2002-US22671	W 20020715
				WO 2002-US22677	W 20020715

AB The present invention relates to compds., kits and methods for detecting a genetic variation in a target nucleic acid, detecting the presence or absence of a particular nucleic acid in a biol. sample, preparing single-stranded nucleic acid probes, and detecting pre-mRNA differential splicing in a target cDNA mol. or a cDNA population. The invention utilizes a nicking endonuclease, extension of 3' termini by a 5'→3' exonuclease-deficient DNA polymerase, and strand displacement for the amplification of a single-stranded nucleic acid fragment containing the sequence of interest. The method may also involve a pair of oligonucleotide primers complementary to sense or antisense sequences located 5' and 3' to the genetic variation of interest. **Primers** contain a nicking endonuclease recognition sequence (NERS) or a **type IIs restriction** endonuclease recognition sequence (TRERS). The method may also involve ligation of adaptor oligonucleotides which contain NERS or TRERS to target DNA. Detection and/or characterization of the amplified short single-stranded nucleic acid fragment identifies the genetic variation of the target nucleic acid, indicates the presence of the particular nucleic acid in the sample, makes single-stranded nucleic acid probes for the nucleic acid of interest, or detects the presence of the exon-exon junction in the target cDNA mol. or the cDNA probes. One example shows detection of 4, 6, 8, and 10-mer oligonucleotides with electrospray-liquid chromatog./time-of-flight mass spectrometry (ES-LC/MS-TOF). Another example shows separation and identification of 8-mer and 10-mer DNA fragments that differ by a single nucleotide (SNP) using HPLC. A cytochrome P 450 2D6 gene fragment containing a polymorphism that is a single nucleotide deletion was separated and identified using LC/MS-TOF with a UV detector. LC/MS anal. was also used to measure allele frequencies of a biallelic single nucleotide polymorphism after amplification of genomic DNA fragments in a complex, pooled sample.

L4 ANSWER 18 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER:	2003:76961 CAPLUS
DOCUMENT NUMBER:	138:148633
TITLE:	Method for analysis of DNA methylation involving bisulfite treatment and DNA amplification with a primer or adaptor containing a nicking endonuclease site
INVENTOR(S):	Van Ness, Jeffrey; Galas, David J.; Van Ness, Lori K.
PATENT ASSIGNEE(S):	Keck Graduate Institute, USA
SOURCE:	PCT Int. Appl., 73 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008623	A2	20030130	WO 2002-US22661	20020715 <--
WO 2003008623	A3	20030501		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
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CA 2492032	AA	20030814	CA 2002-2492032	20020715 <--
US 2003152952	A1	20030814	US 2002-197616	20020715 <--
US 6884586	B2	20050426		
WO 2003080645	A2	20031002	WO 2002-US22674	20020715 <--
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CA 2492423	AA	20040318	CA 2002-2492423	20020715
EP 1470250	A2	20041027	EP 2002-804810	20020715
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EP 1470251	A2	20041027	EP 2002-804811	20020715
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JP 2005516610	T2	20050609	JP 2003-566153	20020715
JP 2005519643	T2	20050707	JP 2004-569980	20020715
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PRIORITY APPLN. INFO.:	US 2001-305637P	P	20010715
	US 2002-345445P	P	20020102
	US 2001-331687P	P	20011119
	WO 2002-US22671	W	20020715
	WO 2002-US22677	W	20020715

AB The invention claims methods and compns. for nucleic acid methylation anal. using bisulfite treatment, an isothermal nucleic acid amplification procedure, and identification of the modified cytosine or unmodified methylcytosine in the amplified DNA fragment. The isothermal DNA amplification procedure involves nicking of a single strand with an endonuclease followed by extension of the 3' terminus with a DNA polymerase, strand displacement, and repetitive nicking-extension reactions. Amplified DNA fragments are characterized at least partially by mass spectrometry, liquid chromatog., and electrophoresis. The method includes treating the target nucleic acid with an agent that differentially modifies a nucleotide based on the methylation state of the nucleotide, forming a mixture of the treated target nucleic acid, a first oligonucleotide primer which includes a sequence of a sense strand of a nicking endonuclease recognition site (NARS), and a second oligonucleotide primer located 5' to the first primer in the target sequence, and amplifying a single-stranded nucleic acid fragment in the presence of a nicking endonuclease that recognizes the NARS. The method also includes

ligating a double-stranded oligonucleotide adaptor which contains an NARS to a treated template nucleic acid and then proceeding with nicking-extension reactions. In an example, oligonucleotide duplexes with mismatches in the recognition sequence for nicking endonuclease N.BstNBI were incubated with dNTPs, trehalose, N.BstNBI, and Vent exo- DNA polymerase. Release of oligonucleotides corresponding to the fragment located downstream (3') from the nicked site on the nicked strand was quantitated by LC/MS. More released oligonucleotides, indicative of more amplification, were observed from duplexes with fewer mismatches within the N.BstNBI recognition sequence.

L4 ANSWER 19 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:866723 CAPLUS
DOCUMENT NUMBER: 137:334024
TITLE: High throughput polymorphism screening in nucleic acid sample
INVENTOR(S): Jones, Keith; Leuther, Kerstin K.; Shapero, Michael H.
PATENT ASSIGNEE(S): SmithKline Beecham Corporation, USA
SOURCE: Eur. Pat. Appl., 28 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1256632	A2	20021113	EP 2002-76698	20020502 <--
EP 1256632	A3	20040102		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
CA 2385144	AA	20021107	CA 2002-2385144	20020503 <--
US 2003082576	A1	20030501	US 2002-139480	20020506 <--
JP 2003009890	A2	20030114	JP 2002-132063	20020507 <--
PRIORITY APPLN. INFO.:			US 2001-289606P	P 20010507

AB Methods are provided for determining the identity of a polymorphic nucleotide in a complex mixture of nucleic acids where one or more distinct polymorphisms can be present in the mixture, and multiple polymorphisms can be screened in parallel. Target nucleic acids are amplified using bridge amplification techniques. The detection and identification of the specific polymorphic residue(s) is based on readout methods that utilize the specificity of specific enzymes for complementary DNA sequences. These approaches result in a labeled nucleotide covalently attached to the amplicon, where the identity of the nucleotide is informative of the polymorphic sequence. In one aspect, the readout process uses primer extension protocols, where the specific base incorporated by DNA polymerase is determined by the sequence at the polymorphic site. In another aspect, the identity of a specific base hybridized and ligated to the amplicon is determined by the sequence at the polymorphic site. The polynucleotide to which the label has been attached can be detected in situ, i.e. bound to the solid substrate used for amplification; or can be released and detected. The author describes a novel method for multiplexed genotyping of SNPs that employs PCR amplification on microspheres. Oligonucleotide PCR **primers** were designed for each polymorphic locus such that one of the **primers** contained a recognition site for Bbvi (a **type IIS restriction** enzyme), followed by II nucleotides of locus-specific sequence, which reside immediately upstream of the polymorphic site. Following amplification, this configuration allows for any SNP to be exposed by BbvI digestion and interrogated via primer extension, four-color minisequencing. Primers containing 5' acrylamide groups were attached covalently to the solid support through copolymn. into acrylamide beads. Highly multiplexed solid-phase amplification using human genomic DNA was demonstrated with 57 beads in a single reaction.

L4 ANSWER 20 OF 39 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:736400 CAPLUS
DOCUMENT NUMBER: 137:258468
TITLE: Modified Serial Analysis of Gene Expression (SAGE) that generates cDNA tags by linker ligation and restriction enzyme cleavage
INVENTOR(S): Yamamoto, Mikio; Yamamoto, Naoki; Hirose, Kunitaka; Kasai, Jun
PATENT ASSIGNEE(S): Kureha Chemical Industry Co., Ltd., Japan
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002074951	A1	20020926	WO 2002-JP2338	20020313 <--
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CA 2455354	AA	20020926	CA 2002-2455354	20020313 <--
EP 1369477	A1	20031210	EP 2002-705113	20020313 <--
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CN 1496402	A	20040512	CN 2002-806623	20020313
US 2004142337	A1	20040722	US 2004-468753	20040310
PRIORITY APPLN. INFO.:			JP 2001-73959 A	20010315
			WO 2002-JP2338 W	20020313

AB A method and kit for construction of cDNA **tags** for gene expression anal. (expressed gene identification (EGI) cDNA **tag**) by using a type II restriction enzyme, two **type IIS restriction** enzymes, and two types of **linkers** X and Y containing recognition sequence for one of the IIS type restriction enzymes, are provided. CDNA is prepared from mRNA using oligo(dT) primers immobilized on latex beads or magnetic beads. DNA chip is claimed. Preparation of cDNA, cleavage with RsaI, and ligation of **linker** X containing restriction site for **type IIS restriction** enzyme BseII, are described. Ligation of linker Y, construction of cDNA library, PCR amplification, and cleavage with BseII followed. The synthesized library was used for anal. of genes whose expression changed upon LPS stimulation.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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                   IPC reform
 NEWS  8  DEC 23   New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                   USPAT2
 NEWS  9  JAN 13   IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
 NEWS 10  JAN 13   New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
                   INPADOC
 NEWS 11  JAN 17   Pre-1988 INPI data added to MARPAT
 NEWS 12  JAN 17   IPC 8 in the WPI family of databases including WPIFV
 NEWS 13  JAN 30   Saved answer limit increased
 NEWS 14  JAN 31   Monthly current-awareness alert (SDI) frequency
                   added to TULSA

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

FILE 'MEDLINE' ENTERED AT 12:35:58 ON 15 FEB 2006
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FILE 'CAPLUS' ENTERED AT 12:35:58 ON 15 FEB 2006
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FILE 'BIOSIS' ENTERED AT 12:35:58 ON 15 FEB 2006

=> S ("type IIs restriction" OR "type 2s restriction") (S) (adapter OR linker OR primer OR tag)
L1 62 ("TYPE IIS RESTRICTION" OR "TYPE 2S RESTRICTION") (S) (ADAPTER OR LINKER OR PRIMER OR TAG)

=> DUP REM L1
PROCESSING COMPLETED FOR L1
L2 51 DUP REM L1 (11 DUPLICATES REMOVED)

=> S L2 AND PY<2003
L3 26 L2 AND PY<2003

=> D L3 1-10 IBIB ABS

L3 ANSWER 1 OF 26 MEDLINE on STN
ACCESSION NUMBER: 2002661789 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12421763
TITLE: Genomic signature tags (GSTs): a system for profiling genomic DNA.
AUTHOR: Dunn John J; McCorkle Sean R; Praissman Laura A; Hind Geoffrey; Van Der Lelie Daniel; Bahou Wadie F; Gnatenko Dmitri V; Krause Maureen K
CORPORATE SOURCE: Biology Department, Brookhaven National Laboratory, Upton, New York 11973, USA.. jdunn@bnl.gov
SOURCE: Genome research, **(2002 Nov)** 12 (11) 1756-65.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200301
ENTRY DATE: Entered STN: 20021108
Last Updated on STN: 20030115
Entered Medline: 20030114

AB Genomic signature tags (GSTs) are the products of a method we have developed for identifying and quantitatively analyzing genomic DNAs. The DNA is initially fragmented with a type II restriction enzyme. An oligonucleotide adaptor containing a recognition site for MmeI, a **type IIS restriction** enzyme, is then used to release 21-bp **tags** from fixed positions in the DNA relative to the sites recognized by the fragmenting enzyme. These tags are PCR-amplified, purified, concatenated, and then cloned and sequenced. The tag sequences and abundances are used to create a high-resolution GST sequence profile of the genomic DNA. GSTs are shown to be long enough for use as oligonucleotide primers to amplify adjacent segments of the DNA, which can then be sequenced to provide additional nucleotide information or used as probes to identify specific clones in metagenomic libraries. GST analysis of the 4.7-Mb Yersinia pestis EV766 genome using BamHI as the fragmenting enzyme and NlaIII as the tagging enzyme validated the precision of our approach. The GST profile predicts that this strain has several changes relative to the archetype CO92 strain, including deletion of a 57-kb region of the chromosome known to be an unstable pathogenicity island.

L3 ANSWER 2 OF 26 MEDLINE on STN
ACCESSION NUMBER: 2001640678 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11691857
TITLE: SNP genotyping by multiplexed solid-phase amplification and fluorescent minisequencing.
AUTHOR: Shapero M H; Leuther K K; Nguyen A; Scott M; Jones K W
CORPORATE SOURCE: Affymax Inc., Palo Alto, California 94304, USA.
SOURCE: Genome research, **(2001 Nov)** 11 (11) 1926-34.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011107
Last Updated on STN: 20020730
Entered Medline: 20011207

AB The emerging role of single-nucleotide polymorphisms (SNPs) in clinical association and pharmacogenetic studies has created a need for high-throughput genotyping technologies. We describe a novel method for multiplexed genotyping of SNPs that employs PCR amplification on microspheres. Oligonucleotide PCR **primers** were designed for each polymorphic locus such that one of the **primers** contained a recognition site for BbvI (a **type IIS restriction** enzyme), followed by 11 nucleotides of locus-specific sequence, which reside immediately upstream of the polymorphic site. Following amplification, this configuration allows for any SNP to be exposed by BbvI digestion and interrogated via primer extension, four-color minisequencing. Primers containing 5' acrylamide groups were attached covalently to the solid support through copolymerization into acrylamide beads. Highly multiplexed solid-phase amplification using human genomic DNA was demonstrated with 57 beads in a single reaction. Multiplexed amplification and minisequencing reactions using bead sets representing eight polymorphic loci were carried out with genomic DNA from eight individuals. Sixty-three of 64 genotypes were accurately determined by this method when compared to genotypes determined by restriction-enzyme digestion of PCR products. This method provides an accurate, robust approach toward multiplexed genotyping that may facilitate the use of SNPs in such diverse applications as pharmacogenetics and genome-wide association studies for complex genetic diseases.

L3 ANSWER 3 OF 26 MEDLINE on STN
ACCESSION NUMBER: 1999403376 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10471752
TITLE: Tandem arrayed ligation of expressed sequence tags (TALEST): a new method for generating global gene expression profiles.
AUTHOR: Spinella D G; Bernardino A K; Redding A C; Koutz P; Wei Y; Pratt E K; Myers K K; Chappell G; Gerken S; McConnell S J
CORPORATE SOURCE: Chugai Biopharmaceuticals, Inc., 6275 Nancy Ridge Drive, San Diego, CA 92121, USA.. dspinella@chugaibio.com
SOURCE: Nucleic acids research, **(1999 Sep 15)** 27 (18) e22.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19990925
Last Updated on STN: 20010521

Entered Medline: 19990915

AB We have developed a new and simple method for quantitatively analyzing global gene expression profiles from cells or tissues. The process, called TALEST, or tandem arrayed ligation of expressed sequence **tags**, employs an oligonucleotide **adapter** containing a **type IIs restriction** enzyme site to facilitate the generation of short (16 bp) ESTs of fixed position in the mRNA. These ESTs are flanked by GC-clamped punctuation sequences which render them resistant to thermal denaturation, allowing their concatenation into long arrays and subsequent recognition and analysis by high-throughput DNA sequencing. A major advantage of the TALEST technique is the avoidance of PCR in all stages of the process and hence the attendant sequence-specific amplification biases that are inherent in other gene expression profiling methods such as SAGE, Differential Display, AFLP, etc. which rely on PCR.

L3 ANSWER 4 OF 26 MEDLINE on STN
ACCESSION NUMBER: 1999068507 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9853618
TITLE: Genotyping by mass spectrometric analysis of short DNA fragments.
COMMENT: Comment in: Nat Biotechnol. 1998 Dec;16(13):1314-5. PubMed ID: 9853606
AUTHOR: Laken S J; Jackson P E; Kinzler K W; Vogelstein B; Strickland P T; Groopman J D; Friesen M D
CORPORATE SOURCE: The Johns Hopkins Oncology Center, Baltimore, MD 21231, USA.
CONTRACT NUMBER: P01 ES06052 (NIEHS)
P30 CA06973 (NCI)
P30 ES03819 (NIEHS)
+
SOURCE: Nature biotechnology, **(1998 Dec)** 16 (13) 1352-6. Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990226

AB A method has been developed to produce small DNA fragments from PCR products for analysis of defined DNA variations by mass spectrometry. The genomic region to be analyzed is PCR-amplified with **primers** containing a sequence for the **type IIS restriction** endonuclease BpmI. BpmI digestion of the resultant PCR products yields fragments as small as seven bases, which are then analyzed by electrospray ionization mass spectrometry. The approach was validated using seven different variants within the APC tumor suppressor gene, in which a perfect correlation was obtained with DNA sequencing. Both the sense and antisense strands were analyzed independently, and several variants can be analyzed simultaneously. These results provide the basis for a generally applicable and highly accurate method that directly queries the mass of variant DNA sequences.

L3 ANSWER 5 OF 26 MEDLINE on STN
ACCESSION NUMBER: 96299639 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8661003
TITLE: Mapping genomic library clones using oligonucleotide arrays.
AUTHOR: Sapolsky R J; Lipshutz R J
CORPORATE SOURCE: Affymetrix, 3380 Central Expressway, Santa Clara, California, 95051, USA.

CONTRACT NUMBER: F32-HG00105-03 (NHGRI)
R-R01-HG00813-03 (NHGRI)
SOURCE: Genomics, **(1996 May 1)** 33 (3) 445-56.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199609
ENTRY DATE: Entered STN: 19961008
Last Updated on STN: 19980206
Entered Medline: 19960920

AB We have developed a high-density DNA probe array and accompanying biochemical and informatic methods to order clones from genomic libraries. This approach involves a series of enzymatic steps for capturing a set of short dispersed sequence markers scattered throughout a high-molecular-weight DNA. By this process, all the ambiguous sequences lying adjacent to a given **Type IIS restriction** site are ligated between two DNA **adapters**. These markers, once amplified and labeled by PCR, can be hybridized and detected on a high-density oligonucleotide array bearing probes complementary to all possible markers. The array is synthesized using light-directed combinatorial chemistry. For each clone in a genomic library, a characteristic set of sequence markers can be determined. On the basis of the similarity between the marker sets for each pair of clones, their relative overlap can be measured. The library can be sequentially ordered into a contig map using this overlap information. This new methodology does not require gel-based methods or prior sequence information and involves manipulations that should allow for easy adaptation to automated processing and data collection.

L3 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:866723 CAPLUS
DOCUMENT NUMBER: 137:334024
TITLE: High throughput polymorphism screening in nucleic acid sample
INVENTOR(S): Jones, Keith; Leuther, Kerstin K.; Shapero, Michael H.
PATENT ASSIGNEE(S): SmithKline Beecham Corporation, USA
SOURCE: Eur. Pat. Appl., 28 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1256632	A2	20021113	EP 2002-76698	20020502 <--
EP 1256632	A3	20040102		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
CA 2385144	AA	20021107	CA 2002-2385144	20020503 <--
US 2003082576	A1	20030501	US 2002-139480	20020506
JP 2003009890	A2	20030114	JP 2002-132063	20020507

PRIORITY APPLN. INFO.: US 2001-289606P P 20010507

AB Methods are provided for determining the identity of a polymorphic nucleotide in a complex mixture of nucleic acids where one or more distinct polymorphisms can be present in the mixture, and multiple polymorphisms can be screened in parallel. Target nucleic acids are amplified using bridge amplification techniques. The detection and identification of the specific polymorphic residue(s) is based on readout methods that utilize the specificity of

specific enzymes for complementary DNA sequences. These approaches result in a labeled nucleotide covalently attached to the amplicon, where the identity of the nucleotide is informative of the polymorphic sequence. In one aspect, the readout process uses primer extension protocols, where the specific base incorporated by DNA polymerase is determined by the sequence at the polymorphic site. In another aspect, the identity of a specific base hybridized and ligated to the amplicon is determined by the sequence at the polymorphic site. The polynucleotide to which the label has been attached can be detected in situ, i.e. bound to the solid substrate used for amplification; or can be released and detected. The author describes a novel method for multiplexed genotyping of SNPs that employs PCR amplification on microspheres. Oligonucleotide PCR **primers** were designed for each polymorphic locus such that one of the **primers** contained a recognition site for Bbvi (a **type IIS restriction** enzyme), followed by II nucleotides of locus-specific sequence, which reside immediately upstream of the polymorphic site. Following amplification, this configuration allows for any SNP to be exposed by BbvI digestion and interrogated via primer extension, four-color minisequencing. Primers containing 5' acrylamide groups were attached covalently to the solid support through copolymn. into acrylamide beads. Highly multiplexed solid-phase amplification using human genomic DNA was demonstrated with 57 beads in a single reaction.

L3 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2002:736400 CAPLUS
DOCUMENT NUMBER: 137:258468
TITLE: Modified Serial Analysis of Gene Expression (SAGE) that generates cDNA tags by linker ligation and restriction enzyme cleavage
INVENTOR(S): Yamamoto, Mikio; Yamamoto, Naoki; Hirose, Kunitaka; Kasai, Jun
PATENT ASSIGNEE(S): Kureha Chemical Industry Co., Ltd., Japan
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002074951	A1	20020926	WO 2002-JP2338	20020313 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2455354	AA	20020926	CA 2002-2455354	20020313 <--
EP 1369477	A1	20031210	EP 2002-705113	20020313
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
CN 1496402	A	20040512	CN 2002-806623	20020313
US 2004142337	A1	20040722	US 2004-468753	20040310

PRIORITY APPLN. INFO.: JP 2001-73959 A 20010315
WO 2002-JP2338 W 20020313

AB A method and kit for construction of cDNA **tags** for gene expression anal. (expressed gene identification (EGI) cDNA **tag**)

by using a type II restriction enzyme, two **type IIS restriction** enzymes, and two types of **linkers** X and Y containing recognition sequence for one of the IIS type restriction enzymes, are provided. CDNA is prepared from mRNA using oligo(dT) primers immobilized on latex beads or magnetic beads. DNA chip is claimed. Preparation of cDNA, cleavage with RsaI, and ligation of **linker** X containing restriction site for **type IIS restriction** enzyme BseII, are described. Ligation of linker Y, construction of cDNA library, PCR amplification, and cleavage with BseII followed. The synthesized library was used for anal. of genes whose expression changed upon LPS stimulation.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:449912 CAPLUS
DOCUMENT NUMBER: 137:28998
TITLE: Labeling of hybridization probes with defined oligonucleotide sequences using overhangs created with type IIS restriction enzymes
INVENTOR(S): Fischer, Achim; Newrzella, Dieter
PATENT ASSIGNEE(S): Axaron Bioscience A.-G., Germany
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002046457	A2	20020613	WO 2001-EP14391	20011207 <--
WO 2002046457	A3	20021219		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
DE 10060827	A1	20020613	DE 2000-10060827	20001207 <--
AU 2002016078	A5	20020618	AU 2002-16078	20011207 <--
PRIORITY APPLN. INFO.:			DE 2000-10060827 A	20001207
			WO 2001-EP14391 W	20011207

AB A method of labeling nucleic acids with probes that have a specific sequence label is described. The method makes use of the variable sequences generated at the ends of cleavage products from type IIS restriction endonucleases. Cleavage products are ligated with oligonucleotides that contain a defined sequence on one end that can be used to address the ligation product to an address on an array. The other end of the probe is a random sequence that will hybridize to one of the possible overhanging ends generated by cleavage with a type IIs restriction enzyme. Alternatively, the two components can be ligated to the cleavage products in sep. reactions. The ligation products are then hybridized to an array and the hybridization pattern analyzed. Variations of the basic method are also described.

L3 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:276116 CAPLUS
DOCUMENT NUMBER: 136:306405

TITLE: Detection of genetic variation by **primer** -mediated introduction of cleavage sites for **type IIS restriction** enzymes with target sequences in the variable region of the cleavage site
INVENTOR(S): Van Ness, Jeffrey; Galas, David J.; Garrison, Lori K.
PATENT ASSIGNEE(S): Keck Graduate Institute, USA
SOURCE: PCT Int. Appl., 135 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002029006	A2	20020411	WO 2001-US42432	20011001 <--
WO 2002029006	A3	20020829		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002011839	A5	20020415	AU 2002-11839	20010928 <--
US 2004019005	A1	20040129	US 2003-398006	20030703

PRIORITY APPLN. INFO.:

US 2000-237409P	P	20001002
US 2000-247166P	P	20001110
US 2000-247167P	P	20001110
US 2000-247172P	P	20001110
US 2000-247173P	P	20001110
US 2000-247275P	P	20001110
US 2001-263971P	P	20010124
US 2001-269244P	P	20010215
US 2001-300319P	P	20010621
US 2001-300350P	P	20010621
US 2001-301394P	P	20010627
WO 2001-US42432	W	20011001

AB A method of analyzing polymorphism at a site in a nucleic acid by incorporating it into the central region of a cleavage site for a type IIS restriction enzyme is described. The method uses a pair of primers, one free and one immobilized with each one carrying one half of the cleavage site. DNA is hybridized to the immobilized primer and the primer is extended and the hybrid is denatured. The second primer then hybridizes to the first extension product, which is immobilized, and is extended. The second extension product then dissocs. from the first extension product and hybridizes to another first primer mol. that has not been extended. The non-extended first **primer** is then extended to form, in combination with the second extension product, a double-stranded nucleic acid fragment that has incorporated the site of interest into a cleavage site for a **type IIS restriction** endonuclease. The single-stranded region of the cleavage product can then be rapidly analyzed to identify sequence variation.

L3 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:158335 CAPLUS
DOCUMENT NUMBER: 136:211876
TITLE: Vectors for cloning genes by self assembly of restriction fragments released by type IIS restriction

enzymes
INVENTOR(S): Hodgson, Clague Pitman
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 12 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2002025561	A1	20020228	US 2001-836737		20010417 <--
PRIORITY APPLN. INFO.:			US 2000-197882P	P	20000417

AB The present invention provides novel vectors and methods for assembling complex DNA mols. starting with a plurality of input gene sequences. The input gene sequences (which overlap with each other by a defined number of bases) are cloned into a vector at a unique restriction site that is flanked on each side by class IIS restriction endonuclease sites. When the clones are digested with the class IIS restriction enzyme, the inserts are released from the vector with a defined number of bases removed from either the 5' or 3' termini, corresponding to the overlap sequences. The overlap sequences, which are unique, non-palindromic sequence strings, permit the fragments to self-assemble. When the fragments are ligated, a seamless, unambiguous linear array fragments is created. The invention can be used for assembling synthetic genes, constructs, vectors and chromosomes. Construction of the cloning vector pWB is described. The plasmid uses a lacZ marker for blue/white screening for inserts.

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